Attorney Doc' No.: BGI-132CP

APPENDIX A: DNA SEQUENCES

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>RXA00010

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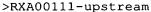
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>RXA00178-upstream

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>RXA00178

>RXA00178-downstream
TAAGTAGAAGCAGCAAAAAACCA

>RXA00226-upstream

 $\tt CCGCCTGCGGTGTCAGCGGAGCGCCCCGGCGTCTGAAAACTGCACTTGGTGAGAACGTGATGTTCATGATGTCACCTGTTCCATCGGTACGGAGGGGC$

>RXA00226

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CTCATGCAGCCCACAATCTCCAGGGCAAAAACGCCCTGATTTTCCGCGCCGACGCGCTC
CAGCCCGCAAGCAGGGGAGCCGACGTCATCATCGCGGACCCTGCCAGACGCGCCGGGGGC
AAGCGCATTACAAATCCGGCACAGCTCCTGCCACCTCTGCCTTCGCTTCTCGACGCCTGG
ATCAACCAACCACTCGCCGTTAAATGTGCCCCCGGCCTTGATTTTTCGGAATGGCCAGGT
CTCGTCAGTATTGCCAGCGTTGATGGAGGCGTGAAAGAAGCATGCCTCTACACTACGGAT
CTGGCAGATGGGGAAACTCGCGAAGCTATCGTGATCAAAGATGGGCTCATTGACCGCATC
ACCAACTTTGAAGACGATGCCACGGGACAAGACCTTGCGGCTGCACCTGGTGAGTTCATC
ATCGACCCAGACGGTGCCATCGTGCGCCGCGGGTTGGTTCGCCACTATGCAGTGCGTGAG
CAGCTGTGGATGTTGGATGAGCGGATCGCATACCTTACGGGCAATCGGATTCCAGAGGGT
ACCAGCGGTTTTAGGTTTATTGAAGAGGTTCCGCTGAAGAAGCTGAAATCGGCGATGGCA
GCACATGATGCGGGGGCGGTTGAAATTTTAGTGCGTGGTGTTTGATGTTGATCCTGATCAG
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GGCAGCCGAGGGGTTGCATTGATTTGTGGTCCTCGCGAGCGCCC

>RXA00226-downstream
TAAAGCCGATGCAAATAAAATTG

>RXA00231

Attorney Jocket No.: BGI-132CP

>RXA00231-downstream TAGCATCTGCCCCTTTACAAATC

>RXA00249

CAGACCCGCCGCCACCTGTCCGTATCGGCTCTGCTGGGCGTACGCACGGTGATCCTCGCA GTCAACAAATTGACCTTGTTGATTACAGCGAAGAGTCTTCCGCAACATTGAAAAGGAA TTCGTTGGCCTGGCATCTGCACTTGATGTCACAGACACCCACGTTGTTCCAATCTCTGCG CTCAAGGGCGACAACGTTGCAGAACCTTCCACCCACATGGATTGGTACACCGGACCAACC GTGCTGGAAATCCTGGAAAACGTAGAAGTTTCCCACGGCCGTGCACACGACCTGGGCTTC CGCTTCCCAATCCAGTACGTCATCCGCGAGCACGCCACCGACTACCGTGGCTACGCCGGC ACCCAGGTCACCCACATCGATTCCGCTGACGGATCCCTCCAGACCGCATCAGTTGGAGAA GCCGTTGTCCTGCGCCTAGCCCAGGAAATCGACCTCATCCGCGGCGAACTCATCGCTGGC GAAGACCGCCCAGAATCCGTTCGCTCCTTCAACGCCACTGTTGTTGGCTTGGCCGATCGC ACCATCAAACCAGGTGCAGCAGTCAAGGTTCGCTACGGCACCGAGCTGGTCCGCGGACGC ACCTACGGCCTCAACGACATCGCACACGTGCGCATCGACGTTGCAGGCGAACTCGAAGTT GAAGATTACGCTGCCCGCGCCCCATCGGATCCTTCCTCCTCATCGACCAATCCTCCGGC GATACCCTCGCAGCTGGCTTGGTTGGCCACCGCCTACGCAATAACTGGTCGATC

>RXA00249-downstream TAGACCAGTGTCTTAGGCAAGAC

>RXA00277-upstream

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>RXA00299-upstream

Attorney Jocket No.: BGI-132CP

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>RXA00299

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AACTCTTACCTCACCGGCCGTTCCCGTCTCCCAGGGGTTAACGCAATTCCAGGCAAGGGC
ACCAACGTACCGCTGTACATCTTGGGTTCATCCCTCTTTGGTGCACAATTGGCAGCACAG
TTGGGTATGCCTTATTCCTTCGCATCCCACTTCGCACCAACTCACCTTGAGCACGCGGTG
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GCCGTCAATGTCACCGCATCTGATTCCACTGAACAAGCCCACGATGATTTCTACAAGGTA
GCGCGTGCACGCGTGAAGAACATGGCATTGCGTGGCCGACAAGTTACTGATGAGCAACTT
GATGAACTCATGGATTCACCAGCTGCTCGCCAAATTGTCGACATGCTTCACTACACCGCT
ATAGGCACTGGATCCCGAAGTTAAAGAATACCTAGACGGTTTTGTAAAGACGGCACAGGCT
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>RXA00299-downstream TAGTACCGATGGGCCGGTAGACA

>RXA00332-upstream

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>RXA00332

>RXA00332-downstream
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>RXA00354

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TTTTATCTCGAGTCCAACAACGGTTTGTATGCAAGCCGTGGTTTCCGTGAGGCTTCTAAG
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TCTCAGGAAGATTTGGACGCAGCGCGTGAGGCGTTCCCTAACCTGGAGCACACCACGTGG
GGTGGTCAGACGGGTGCGTTGTTCGGCACGATCGGTGTCTCTCAACAAGAAGATCGGC
GTGGATCGCCTGCTGAAGTACCTGAACGCAGATCGCCCAAACACCATTGCGTTCGGCGAC
AGCGATGAGGATCTCTCCCTATTTGAGGCGAGCGCTTACGGCGTCGCGATGGGCGAGGCC
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>RXA00354-downstream TGACCCCATCAAAGAACTTCCCA

>RXA00372-upstream

Attorne, Jocket No.: BGI-132CP

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>RXA00372

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>RXA00372-downstream TAGTTTTCCTATGCAGTTATCTC

>RXA00470-upstream

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>RXA00470

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>RXA00471-upstream

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>RXA00471

>RXA00471-downstream TAATGGCGGCTAAAAAGGTGGC

>RXA00499

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>RXA00499-downstream TGATTCCTCGTGTTAGTACTAGC

>RXA00500-upstream

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>RXA00500

>RXA00500-downstream TGAGTGAACAATTCGAGCTACGG

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>RXA00501-upstream

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>RXA00501

>RXA00501-downstream
TAAACCATGATCGTTTTGGGAAT

>RXA00502-upstream

>RXA00502

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>RXA00502-downstream TAAACATTTAGTATTAGTTCCAT

>RXA00566-upstream

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>RXA00566

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>RXA00566-downstream TAGAGTTTTTTAAAGATTCGGGT

>RXA00567-upstream

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>RXA00569-upstream

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>RXA00569-downstream TGATCGATTCCCCCGCCTCTATC

>RXA00594-upstream

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>RXA00594

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>RXA00612

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>RXA00612-downstream TAGAAATACCTAGTTGCTCAAAC

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>RXA00615

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ACCCAGGCAACTTTGTTGGGTTATGTGGGCGGATGCTTTTCCAAGAACAACCGTTGATC
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Attorne, Jocket No.: BGI-132CP

>RXA00621-upstream

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>RXA00621

>RXA00621-downstream TGAAGTACGCGTGCTTCCTTTCG

>RXA00622-upstream

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>RXA00622

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>RXA00622-downstream
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>RXA00636-upstream

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>RXA00636

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>RXA00641

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>RXA00650-upstream

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>RXA00650

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Attorne;)ocket No.: BGI-132CP

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>RXA00658-upstream

>RXA00658

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>RXA00659

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>RXA00663

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>RXA00675

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>RXA00689

>RXA00689-downstream
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>RXA00744

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>RXA00773-upstream

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>RXA00773

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>RXA00778

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>RXA00787-upstream

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>RXA00787

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>RXA00791

>RXA00793-upstream

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>RXA00793

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>RXA00793-downstream TAGATCACGGATCGGCTGCTTTA

>RXA00797-upstream

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>RXA00797

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>RXA00820-upstream

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>RXA00820

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GCT

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>RXA00833-upstream

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>RXA00833

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>RXA00844-upstream

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>RXA00906-upstream

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>RXA00912-upstream

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>RXA00912-downstream TAAATGACCCTGCAACTATTCAC

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Attorney locket No.: BGI-132CP

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>RXA01059-upstream

>RXA01059

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>RXA01059-downstream TAGAAACCACTCTAGAAATAGCT

>RXA01073-upstream

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>RXA01082-upstream

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>RXA01082

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>RXA01090-upstream

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>RXA01090

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>RXA01117

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>RXA01117-downstream
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>RXA01120-upstream

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>RXA01120-downstream TAGTTGGCAGGAGTTATCACCGG

>RXA01224-upstream

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>RXA01224

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>RXA01126

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>RXA01147-upstream

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>RXA01151

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>RXA01571-downstream TGAGGTTACCGTTCTGTCCCGTT

>RXA01161-upstream

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>RXA01161-downstream TGAGCATTCTTCTCCTAGGCGGA

>RXA01181

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>RXA01192

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>RXA01192-downstream TAAACGGG

>RXA01214-upstream

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>RXA01224-upstream

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>RXA01250

>RXA01254-upstream

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>RXA01288

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>RXA01302-upstream

>RXA01302

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>RXA01303

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>RXA01458-upstream

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>RXA01511

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>RXA01513-upstream

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>RXA01513

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>RXA01589

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>RXA01603-upstream

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>RXA01603

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>RXA01607-upstream

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>RXA01608-upstream

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>RXA01609-downstream TAAAAACGCCTAGGCCACAAGCC

>RXA01620-upstream

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>RXA01620

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>RXA01654-upstream

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≯RXA01728-downstream TAAATAATGAGTAAAAAGTCTGT

>RXA01795-upstream

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>RXA01795

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>RXA01802-upstream

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>RXA01802

>RXA01802-downstream TAACGATTGCAGGCAGCAGGTTC

>RXA01828-upstream

>RXA01828

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>RXA01828-downstream
TAAAATATGAGTCAAGAAGACAT

>RXA01829-upstream

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>RXA01829

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>RXA01829-downstream TGAACCGCTCGATTCGAATCACA

>RXA01838

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>RXA01838-downstream TAGTTTTTCTGAAACTAAGGAGA

>RXA01848-upstream

>RXA01848

>RXA01848-downstream TAGACAACCAGAGTGAGGGTTTC

>RXA01849

>RXA01849-downstream TAGGCATTTGCGCCTGGCGTCCA

>RXA01868-upstream
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>RXA01868

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>RXA01868-downstream TAGTTGTTAGTTGGTATTGAAAA

>RXA01869-upstream

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>RXA01869

>RXA01869-downstream TAGGTTTCTGGGTGGAGAAGGAT

>RXA01885-upstream

 ${\tt GTGGCGTCGCAGGGATGTTCCTGCGGCACCATTTTTGCTGAGGTGGAACTCACGGATTAAACACGGATTTTTCTAAGGTTAATCAAGTAAGGTTTACCTT}$

>RXA01885

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>RXA01885-downstream TAGGGATCTGAAATGGAGGGGTG

>RXA01914-upstream

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>RXA01914

>RXA01918-upstream

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>RXA01918

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>RXA01918-downstream TGAGTTCTAGCAAATGGCGGCTT

>RXA01932-upstream

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>RXA01932

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>RXA01933-upstream

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>RXA01933

>RXA01933-downstream TGACACCTCAACCACTGATTTTG

>RXA01934-upstream

>RXA01934

>RXA01934-downstream TAAGTGGCTCGTTGAGTAGTCGA

>RXA01967-upstream

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>RXA01967

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CTC

>RXA01967-downstream
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>RXA01971-upstream

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>RXA01971

>RXA01971-downstream
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>RXA01993

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>RXA01993-downstream TAAACCATGAACTCGCAATGGCA

>RXA01994-upstream

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>RXA01994

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>RXA01997-upstream

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>RXA01997

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>RXA02000-upstream

>RXA02000

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>RXA02010-upstream

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>RXA02010

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>RXA02012

>RXA02016-upstream

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>RXA02016

>RXA02016-downstream TAAATTCCTCACAAGCCCCCTAG

>RXA02017-upstream

>RXA02017

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>RXA02017-downstream TAGGACACACTATGTCAAACTTT

>RXA02018

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>RXA02018-downstream
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>RXA02048-upstream GCGCGGCGGATAACAAGCAGACCGCGTTTGTGGAATCGCTGATCTACACCTGGATCGAAA AGACTTTGGATCAGCAGGGTAGCATTTAATACCTATGATT

>RXA02048

ATGCGAAGGCTGCGCTCCACCCCGGTCCCTGGTACACGCGATTCCTACACAGGAATTGAT TTCAACTTAGGCTTCCACATCCGACGCTACGAGCTTGATCTCACCTACCGCGTAGCACCC **AACCTGCTCATGGGCACCGCAACGCTGCACATGGATAATTACCGTGCGCTCGACGCGCTG** ACCCTGGACCTCGGCGCAGCCTGCGCGTGGAAAAAGTCACCGCCAAAGGCACCGCCGGC ACCCACATCCAAGTCGCGCGCTTCCGCCACGCCGGCCGCAAACTGCGCATCACCTTCCGC AACCAAATCCCGGTTGACCAGGAATTTTCACTCACCATCCGCTACCGCGGCAACCCGCGC CCCCTGCGCAGCGAATGGGGCATGATCGGCTGGGAAGAGCTCGACAACGGCGCCCTCGTC GCCGCCCAGCCAAACGGCGCGCGAGCTGGTTCCCCTGCGACGACACGCCCGACGAGAAG GCGCTTTTCGACGTCCACTTCCACACCGACAACGGATACGCCGCCATTATCACCGGTGAT TTAATCTCAAAACACGTCAGTGGCAGCATGACCACCTGGCACTACCAATCCCGCGAACCC ATGGCCACCTACCTCGCAGCCGTCCACGTCGGAGAATACGACACTGTATCCCTGGGCGTT TCGGAATCGGCCTTGTGGTGGAGGCGTATGTGCCTGTGGGGGATGCGGCCTTGCGGGCT CGGATTTTGGAGGACTTTGCCAAACAAGTCGACATGTTAGACGCCTACGAAAAACTCTTC GGCCCTACCCATTCCGCAGCTACCGCGTAGTCATCACCGAAGACGAACTCGAAATCCCA CTCGAAGCCCAAGGCCTCTCCAGCTTCGGAGCCAACCACGCCACCGGCGAAGGAACCTGG CAATGGAACGACATCTGGCTCAACGAAGGCTTCGCCTGTTACGCGGAATGGCTCTGGTTT GAGGCAGCTGGAGTTAAGTCGGCTGCGGAAAGTGCGTTGGAATTCTATCGAGGCCTGGAG GCGCTGCCGAAGGATATTTTGCTGGCCAACCCCGGCGCGAAGGATATGTTCGACGACCGC GTCTACAAGCGCGGCGCTCTGACTGTCCATGCATTGCGGGAATTGCTTGGCGATGATGCA TTCTTCAAAGCTGTGCGCTCCTACGTTGCCGAAGGCCGACACGGACTCGTTGAACCCCGC GACCTGAAACGACACCTCTACGCAGTCTCCACAGACCACGCAGCTTTAGATGCAGTGTGG CAGTCCTGGCTTCGCGATCTGGAGTTGCCGGAGTTTCCTTCTGGTGGTTTGGAC

>RXA02048-downstream TAGTGCGCTATCTGACGCTGGCC

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>RXA02052-upstream

>RXA02052

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CTCGACGCACTTTTGGCTTTTGGGAATTACTCCAGTCGGAGCTACGGAATCTGGATCCGAA
AATGGTTTCCCCGCCTACTTGGCTGACGAGCTAAAAGACACCGAATCTGTTGGGCTGACA
TCTGAGCCAAATTTGGAAAAGATCGCCGCACTGGATCCGGATTTGATCATTGGCGCAAAG
GTCCGCCACGAGGCTATTTATGATCAGCTTTCAGACATCGCACCAACCGTGATGTCCGAA
GGTTCCGGCACAAACTGGAATGAACAGGCAGAAATCACTGCGCAGCAGCAGTAAACAAGTCT
GATGAGATGGACAAACTGATCTCAGACTTGGACACCCGTGCCACAGAGCTTGGTGAAGAG
ATCGGTGCTGACGGACAAACCGCTTCAATGGTTCGATTCCGCACGGACAACTTCAGGCTC
TATGGTCCCGAGACCTTCTCTGGTTCAGTTCTGGAACAAGTTTGGATTTGACCTGGGGGAA
CGTGATTGGAATGAGTACTCCATGATGGAGCTATCCTCAGAAAACTTTTGGGCAGATCGAT
GGAGACCTTATTTTCTACACCATCCCAGGATCCCCTGAAGCAACCTTATCCAAAGATT
TCCGAACTGTGGGTTGATTCACCAGCAGTTCGGCAAGGTAGAACTTACGAGTTTGAAGAC
GAAACCTGGATGGTCGGCATCGGTGTATTAGGTGCCAATGAAATCTTGGATGACCTGGAA
GAAACCTGGATGGTCGGCATCGGTGTATTAGGTGCCAATGAAATCTTGGATGACCTGGAA
GAAACTCTGAGC

>RXA02052-downstream TAGTTTCCTTTAGGCCAAGCAAC

>RXA02064-upstream

>RXA02064

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ATCGCGATTACCCCGGCTGCCGGGTTGGTGGGTCTGTATATCCTGAACGGACTGGCCGAT
AACACCACACTGACCTGCATTGATCCTGAATCAGAGCATCAGCGCCAGGCCAAAGCACTC
TTCCGCGAGGCCGGCTATTCCCCCAGCCGCTTCTTTGCTCTCGCGCCCGCTCGAC
GTGATGAGTCGCCTTGCCAACGACAGCTATCAGCTTGTTTTCGGCCAAGTCTCCCCCATG
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CTCGCCGATGCGCTCCTTGACGGCACCATTGCGGATCAAACCCGCAAGGATCGTGACAC
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>RXA02064-downstream
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>RXA02083-upstream

 ${\tt TTTTTGTACATGGTCTGTGGCACGCATTGTTTCGTTTGCCCTGCCATGTTGGTGTTTTAAGTGAAGGCCGCCTTTTGCGGAATGGGTATAGGAGGCATTC}$

>RXA02083

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GACTCTTATGGTGAGCCTGTGCACTCAAGTATGTACCGAAACCTGTGGTCAAACGGTCCG
AAGGAAGTTCTCGAATTTGCTGAGTACAGCTTCGATGAGCACTTCGGAAAGCCAATTTCT
TCTTACCCTCCACGTGAAGTGTTGTGGGATTACATTGCAGGTCGTGCAAAGAAGTCGAAC
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>RXA02083-downstream TAAGGAAAAGGCCTAAGCAGCCC

>RXA02092-upstream

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>RXA02092

ATGGCTAACAGTGCAGCGGGTTCGGTGTTGGCGGATGAGATGGTGGTTCCCACCTCAACA GGGTTTGTTAAAGGCGTCAAAGGACCAGGGCTTAAAACCTGGAGGGGAATTCCCTACGGC CGAAACACTGGCGGAAAATATCGCTTCCGGGCACCCCGGCCCCAAGAAATGGGACGGC GTGCGCGATTGCTCAATGTTCGGTGAAGTAGCTTCTCAGCCAACGTACTCCTGGACAGAT AAGATTCGCGGTTCAGAAGACTGCCTTAACCTCGATGTCGTGCGGCCTGATTCCGAAGAA AAGCTTCCTGTTGTGGTGTATCTCCACGGCGGTTCCTTCATCATGGGCTCATCAAGCGAA AAAGCGCTGCGCGGATATAACCTCGTCACAAACATGAATGTGGTCTACGTGTCCGTTAAT TTCCGCCTCGGCGCTTTGGGCTATCTAGATCTGCGTTCCGTGGGGGAGGATTGCGTAGCC AACCCGCGCTCCACGATCAGCTCCTGGCCCTGCAGTGGGTCAGCCGTAATATCAAAGCA TTCGGTGGGGATCCTGACAACGTCACCCTCATGGGCGAATCCGCGGGCGCTGCAGCAGTG GTTGCACTCATGTGTGCCCGCTGCAGGAGGACTATTCCACCGCGCCATCGCCCAATCC GCGCCGGTCATCTGTGCACTCATCTACCCAAGCAAAATTCTGGGCACGTGAACTGATC TACCGCATGGCATTGCCCAGGGAAACCACCTTGGATGAACTGCGCCAAGAATCCGCCGAT GATCTAGTGCGCCCGGGCAGTCGATGATGTGGCGCTCCGGCGAACTGCTCCAACTCAAC TCTTGTTACGGGCCCACGGTGGATGGTTCCTTGCTACCTGAGCACCCGCTCACCATGTTT GAACAGGGAAGACACCGCATTCCCTTCATGATCGGTACTAATAACGGAGAAACTTCT TTCTCCAAAGCCTTTTATTTAAGAAGCTCTGCCCGACGTCGCTCTGCCTTACGCATGCTG TCTGTGTATGATCCCCACAATGCAGAACGCGTGGTTAGCGCCTATGGCGGAGGCGAGGCA CGCACAGACTTTTCTGAACTACTCGCTGACGCGCTGTTCTGGGCACCGTCGGTTAGATTG GCGCAGTCGCACGCCTCCCAAGATGAAGATACCTGGATGTACCGCTTCGATTACGCCCCA CAATCCATGCGGAAACTTGGCCTCGGCGCGATTCACTCTTTCGAACTCAACGCTGTCTTT GGCGATCATGAATCTTCTCGCTCCATGAACCTTGCGAAAATTGCCGGCGGCATGGATCAT TTGGATAAAGTCACCGAACTTGTCCAAGAGCATTGGAAGCAATTCATCTACTTCGGCAGG CCCGGTGAAGAGTGGAAGGCTTACCGCGGCCGCAGCGATACCGAACCGGGCCGTGCTACA TTTGTCATCGATATCAACTCCCGAATCGCGTGGGATCCACGCCAGGACAAACGCACGGCG TGGGAAAATTACGACATGCTCGAATGGGGCACAGGCCGCCCAGATCTAGCCAACGAACTT GATTTCATCGAGCCGGAAGAGACAGAAGAGAGCAGCAATTGAAGTGGCTTAGCCTTATG CAGTTTTTTGGAAGTAGA

>RXA02092-downstream
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>RXA02098-upstream

 ${\tt CCCCATTTCGGCGACCTCGACTCCATGAAAGCAAGAGTTTCACCACATTTAACGTGGGGT}\\ {\tt ACCTGTGTGCATCGGGGTCAAACCTGCCACTATAGAGGGT}\\$

>RXA02098

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>RXA02098-downstream TAGAAACCCGATAAGCGAGAACC

>RXA02101-upstream GCCATGGAATGCTCCGTTGAACGCAACAGCCTTAAATACAATCCCCTCCTATAAGCCAAG AGTTTTAGTGTCGCTGCGCAGGTACTCTACTATCTAATCC

>RXA02101

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>RXA02105-upstream

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>RXA02105

>RXA02111-upstream

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>RXA02111

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>RXA02111-downstream
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>RXA02118-upstream

 ${\tt GGGCTGGTGCGGTTGCTTTAATGGAGGTCATGCTCGCAGGCTAACAGAATTGGTGGTTT}\\ {\tt TAGTGCTGTTACCAGGGACATCGGCTAGAATCTGCTGAAT}$

>RXA02118

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>RXA02118-downstream TAAACCCTTTTAAGGAGCTTTAG

>RXA02120-upstream

>RXA02120

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AACATGAATTTTGCAGATTATATGGCGGTGGTCAAGAAGATCACCTCGGCGGTATCCATC
CCCGTAAGCGTTGATGTGGAATCCGGTTATGGTCTCTCGCCTGCGGATTTGATCGCACAG
ATTTTGGAAGCTGGCGCAGTGGGCATCAATGTGGAAGATGTTGTGCACAGCGAGGGTAAG
CGTGTTCGTGAGGCGCAGGAGCACGCTGATTACATCGCTGCGGCACGTCAAACTTGGTGCAGAC
GTTTTTGAAGATCCGATGGTGATCAACGGTCGCACGATCAAGCTCATGGAACAGCCAGGC
GCGCGTTCGGTGTACCCCGTGGGTCTGAGCACCCCCGAGCAGGTTGAGCGCCTGGTGGAC
GCTGTGTCAGTGCCGGTCAACATCACCGCGCACCCCGGTTGATGGCCCCGCGCACAAAAA
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>RXA02120-downstream TAAATTGCTTGTCGACGCCTAGT

>RXA02126-upstream

>RXA02126

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>RXA02126-downstream
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>RXA02192

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AACGCTGCTCTTGAAGCCGGCTATCGCCACATCGACACCGCGGCCGCATACGGCAATGAA
CGTGAAGTCGGTGAAGCAATCGCAGCATCCGGCATTGGCCGCACGAGATCACCATCGAA
ACCAAAATCTGGGTGACCGACTACGGCTTCGAGGAAACTCTCCACGCATTCGACAAGGCC
ACAGGCAAGCTTGGTGTCGATACACTGGACATTTTGATCTTGCACCAGGCAGTGCCAAGC
AGCTTTGATCGCACCATCGCCGCCTACAAGGCGCTAGAGAAGCTGCTTTTCGACGGCGCG
GTGCGGGCAATCGGAGTCAGTAATTTCATGCCAGAGCACCTGGACAAACTCCTTTTGGAA
ACCTCCATTGTCCCAGCTCTGAACCAAATCGAATGCCACCCCTACTTCCAGCAGCGTGAC
GTGCTTGCCCGCAATGAGCAGCTTTGGCATTTTTGACTCAGGCG

>RXA02214-upstream

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>RXA02214

>RXA02214-downstream TAACCCTGAAGGCGATTTAAGGG

>RXA02215

>RXA02215-downstream
TAATAAGGCACCATTTGGATGGT

>RXA02264-upstream

 ${\tt TCCCTGACATCCAGGTTGAAGCAACGTTTGATGACGGCACCAAGCTCGTCACCGTGCACAATCCCATCCGATAACCCTTGATGTTTTTAGGAGTTTTTGTC}$

>RXA02264

>RXA02265-upstream

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>RXA02265

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TATGAACTGATTGAAGGCGCCCGTGACGGACGCACAGTCGCAGACCTTATGAGCTGGGGA
AGCACCATTTTGACTAGGGATGATGTCTTAGAAGGCATCCCAGAGATGATCCCTGACATC
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>RXA02265-downstream
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>RXA02274

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>RXA02274-downstream TAATCCGCCAACAAGGAAGGAAG

>RXA02275-upstream

>RXA02275

>RXA02275-downstream TGATGGATCTTGACGCTGATTTT

>RXA02276-upstream

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TTCCGCCAATTCCTTTCAGGCATAGCGGCACACACATTG

>RXA02276

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>RXA02277-upstream

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>RXA02277

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GTTGGCATTGAAACTGGAGGATGCCCACACACTGCGATTCGTGAAGACACCTCCATGAAT
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TCTGGTGGAGATAATCTCTCTGCAACGTTCTCGCCAGAGCTGGTGGATTTTTCCATCTAC
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GTCATGGTGGAAGATGCCAAAGCATTCCGCAAGAACAAACCATTCTGCCTGACTAATCTG
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GACTTGCAGGAAGCC

>RXA02277-downstream
TAAATGACACAAACCCAACCAGT

>RXA02278-upstream

ACCATTCTGCCTGACTAATCTGCGCACCGATGATGGTTTGGATAAGGTCTTGGAATGGATCCGCCATGAGGTGATGATGCAGGACTTGCAGGAAGCCTAA

>RXA02278

>RXA02278-downstream TAGACGCCGTCGAGAAATCGAAG

>RXA02316-upstream

Attorne; locket No.: BGI-132CP

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>RXA02723

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>RXA02745

>RXA02745-downstream
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>RXA02746

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>RXA02828

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>RXA02839

>RXA02855-upstream

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>RXA02859

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>RXA02895-upstream

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>RXN00073

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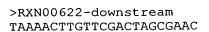
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>RXN01226

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>RXN01267-upstream

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>RXN01267

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>RXN01277

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>RXN01653-upstream

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>RXN01653

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>RXN01716-downstream TGAAACCGAAGTGGAAATCGCCC

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>RXN01842

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Attornel locket No.: BGI-132CP

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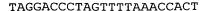
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>RXN03091-upstream

>RXN03091

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>RXN03091-downstream TGAAGGTTCCTTCGACGGCGAAA

>RXN03092-upstream

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>RXN03128

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>RXN03131-upstream

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>RXN03131

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>RXN03133-upstream

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>RXN03133

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>RXN03133-downstream
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>RXN03145-upstream

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>RXN03145

>RXN03145-downstream TAGCTCTCGAATAGGCCATTTCT

>RXN03178

>RXN03178-downstream TAGGTGTTCTTCTTCACGACCTC

>RXN02021-upstream

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RXC00110 - 5'-Region

RXC00110 - coding Region

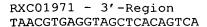
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RXC00110 - 3'-Region
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RXC01971 - 5'-Region

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RXC01971 - coding Region



RXS00004 - 5'-Region

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RXS00004 - coding Region

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RXS00004 - 3'-Region TGAGGGCACCGCAAGCGTGGCGC

RXS00156 - 5'-Region

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RXS00156 - coding Region

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RXS00156 - 3'-Region TAGGAGTGATAGTCCCTCGCAAA

RXS00166 - 5'-Region

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RXS00166 - coding Region

RXS00166 - 3'-Region TAGGAGCCCTCGCCATGTACCTG

RXS00197 - 5'-Region

RXS00197 - coding Region

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RXS00197 - 3'-Region
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RXS00288 - 5'-Region

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RXS00288 - coding Region

RXS00288 - 3'-Region TAAAGAGGACTTGAAAAATGCAC

RXS00624 - 5'-Region

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RXS00624 - coding Region

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RXS00624 - 3'-Region TAGTTGGGGAGGTTCGGGGCACC

RXS00949 - 5'-Region

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RXS00949 - coding Region

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RXS00949 - 3'-Region TAAAGACGAAAAGAGGGAGAATG

RXS01000 - 5'-Region

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RXS01000 - coding Region

RXS01000 - 3'-Region TGACGCTCCACCAAGCATCCGCA

RXS01002 - 5'-Region

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RXS01002 - coding Region

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RXS01002 - 3'-Region TGACCACGCCTTCTTCTACACTT

RXS01003 - 5'-Region

RXS01003 - coding Region

RXS01003 - 3'-Region TGAGCACCTTAACCTCTCACCGC

RXS01114 - 5'-Region

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RXS01114 - coding Region

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RXS01114 - 3'-Region TAAAAATGGCTATTTTGCACAGC



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RXS01205 - 3'-Region TAAGTGATTGTCACTTTGGATTG

RXS01223 - 5'-Region

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RXS01223 - coding Region

RXS01223 - 3'-Region TAGATTGCTAGAGATTCCCGCAC

RXS01269 - 5'-Region -

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RXS01269 - coding Region

RXS01269 - 3'-Region TAGCAGGTAAAAATTTTACTTTC

RXS01421 - 5'-Region

RXS01421 - coding Region

RXS01421 - 3'-Region TAAAGCTGTGGCTGCGGAATGCG

RXS01491 - 5'-Region

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RXS01491 - coding Region

RXS01491 - 3'-Region TGAACTGGATGGAGAGGATACCT

RXS01572 - 5'-Region

RXS01572 - coding Region

RXS01572 - 3'-Region TAGGTTTACTGAAGTTCAGACTT

RXS01642 - 5'-Region

TTGGAATCACTGTGTCTTGCAGCTAGTCTGCCACTCGCACTGCATTTGCTGGATGTATTTGGAATGCTGCGCGGTCTTGATATTGGATTCGGTGGATAAG

RXS01642 - coding Region

ATGCGCAGACTCATCGCGGTTAGCTTGGCCGCTCTGTTTATGTTGGCTTCCACTCCAGCGACGAGGGCA CACCTTTCGCAGTCATTATCCCAAGCTCACCAACTAGCAACTGGCGCCGGTGTGATGGTGGCAGTCATC GACACCGGAGTATCCCTGCATCCACGTCTGCCCCACTTAATTCCCGGCGGTGATTTCGTGGGCGCCCAC CAAAGCCCCGATGTGCCAGGTGAACTTATCGATTGCGACGGCCACGGCACCATCGTCGCCGGAATCATC GCCTCCCAAGGAAACCCCGGCACCGGCTGGCCATATGACGGCAGCTCCGATCCTTATATCGGTGTCGCC CCAGATTCCGGAATCATCTCCATTAAACAAACCAGCTCATATGTGCGTACTCGTGAAGATTCCAACGTC GGAACGCTGAGCACCCTGGCGGAATCCATCCACCGAGCTCTCGATTCCGGTGCCCACGTGATCAATATT TCCGTGGTGTCCTGTTTGCCCCAATCACCCGACGAGGCCGCATCGTTCCAGCCTCTGACGGATGCTCTT AACAGAGCAGAACTTCAAGGGGTGATAGTGGTGGCAGCAGCAGGAAACCTCGGGCAGGATTGTCCAGTT GGATCTACCGTTTATCCTGCACATTCAGACACTGTGCTCTCTGTGTCGGCACGTTTTGATTCTCACACG CTTGCAGAATATTCCATGCCTGGCAACCAACAAATCCTCTCTGCACCAAGCCACATTCAGGCTGGTCTA TCACCGCGTGGCGACGGCTTCGCCAGCCACATGATCACCACCGCTGGCGAAAGCCCCTTCGAGGGCACC AGTTTTGCCGCTCCAGTTGTCAGCGCCACAGCTGCACTGCTTCGCCAGCATTTTCCCTTTGCCACACCC TATGAAATTCGTGCACGAATCTTCAACAGCATCGACCCTGCAAGAGGCGCTATTGATCCCTACCTGGCA CTTACTCAAGAAATCTATCCCACCACTCCCTGGTTCATGAGATCGCACTAAGTGTTCCCACGCCGCCG GATGATTCTCCACGGGAGCGGGCATCCTAGTTACCGCAATCATTGTTGGGTTGCTCGCAGTGTTAGCT

RXS01642 - 3'-Region

TAATCTATGAGGCACCGTTCAGA

RXS01902 - 5'-Region

GGCTGGTCCGAAGTGCAAACCTTCAACACCGGCACCTACGGTGACAACTGGAACTTCCTCTTCTTCGGCGACACCCAGCTGTACAACACCCCACTCCAACC

RXS01902 - coding Region

GTGCAGAAGACTCCAGAACTGGGCAAACAACCTGGAACGGCGCCCACCAATCGAAAACCCAGGAACC TCCTTCATCCTCTCCGCGGGTGATCAGGCAAACCACTCCAGCTGGGACGAGCACTCCGCATACATCTCC CCAGAAACCCTGCGCAACTACCGTCTGGCCGTGAACAATGGAAACCACGACCAGTACAACTACGACGCC TACAACGCGATGTACCCACGCCCTAACCAGGTCGATGAGAACTACTTCTTCGAGTACAACAATGCACTC TTCCTGTCCCTGGACTCCAACGACTACTTGGACATCGACGACGACATCGCATTCCTTCGCGACACCGTC GCAGCACACGGTGACGACAAGGACTGGATCGTCCTGACCTACCACCATTCCACTTTCTCCCAGGCCTAC CACATGGATGACGCTCGCATTAAGTACCAGCGCGAACGCCTCACCCCAGTGATCTCTGAACTGAACGTT GACTTGGTTCTCGGTGGACACGACCACATCTACACCCGCTCCCACCTGATGAACGGCTTCACCCCAGTC GATGCAGGCCGCGAAGCAGTTGTCGGTGAAACTCTGAACCCTAAGGCCGGCGAAGTTGTTTACCTTGCA ACCAACTCTTCCTCAGGCTCCAAGTTCTACGACTTCTACGACTTCCAGCTCGGCCAGCGTTACGACACC GGACTGGATTTCCAGGAAACCGTCGATCAGAAGAAGATCCGCACCTACACCGCAGTCTGGAACCAGGAC CAGGTTCAGGACTACACCAACGTTGAACTGACCCCAGAAGGCCTGACTGTGACCACTAAGGACGCAGTC TCCGGCGAGCTGGTTGACCAGTTCACCCTGAGCAAGCAGGACCGCGACGAAGAATCTGAAGTCCCAGTT GAAGATGACAAGGACGGACAACGCGACCGGCTCCTCCAACCTTGGTCTAGCTGCTATCTTGGCTCCA GTTCTGGCCATCTTCGGTTCGTCGGTGGACTCTTTGTTGGCGGCGGCTCCCTCGCTGAGTTCTTTGCC AACCTCGGCGTGAAGATGCCTTTC

RXS01902 - 3'-Region TAATACTGTCTGAGATTCAAGCA

RXS02453 - 5'-Region

AACCAACAAAGGTCATCTCAACCGGCTTAAGAAAATTCTGCCAGCTTTCTGCTGATTGAATCGTGCCAGCTCAGGGCATATCTCACCTAAAGTAAACACC

RXS02453 - coding Region

RXS02453 - 3'-Region

 ${\tt TAAATGAATTGATTATTTTAGGC}$

RXS02474 - 5'-Region

RXS02474 - coding Region

ATGAGCAAAGTTGCAATGGTTACCGGTGGTGCACAAGGCATCGGTCGTGGAATTTCAGAGAAGCTGGCA
GCAGATGGTTTCGATATTGCCGTAGCCGACCTGCCACAACAGGAAGAACAAGCTGCAGAGACCATCAAG
TTGATTGAAGCTGCAGGTCAAAAGGCTGTATTCGTTGGATTAGATGTCACCGATAAGGCTAATTTCGAC
AGTGCAATTGATGAGGCAGCAGAGAAACTTGGCGGCTTCGATGTGCTAGTAAACAACGCCGGCATCGCA
CAAATTAAGCCACTTCTGGAAGTCACCGAAGAAGACCTAAAGCAGATCTACTCCGTGAACGTTTTTAGC
GTATTTTTTGGTATTCAAGCAGCATCCCGAAAGTTCGATGAGCTTGGCGTAAAAGGCAAGATCATCAAC
GCTGCATCAATCGCTGCTATCCAAGGTTTCCCAATCTTGAGCGCCTACTCCACCACCAAATTCGCGGTT
CGTGGCCTCACCCAGGCTGCTGCGCAAGAACTCGCACCCAAGGGTCACACCGTGAATGCCTACGCACCT
GGCATCGTGGGCACCGGAATGTGGGAGCAAATCGATGCCGAGCTTTCCAAGATCAACGGCAAGCCAATC
GGTGAGAACTTCAAGGAGTACTCCTCCTCAATCGCATTTGGGCCGACCATCAGTACCTGAGGATGTAGCC

GGTCTGGTTTCGTTCCTGGCTTCTGAAAACTCCAACTACATCACCGGACAGGTCATGCTTGTCGACGGCGGCATGCTCTACAAC

RXS02474 - 3'-Region TAGGGGTTGCTTTCCCGCACTCA

RXS02485 - 5'-Region

RXS02485 - coding Region

TTGGATTCATCGCTAGCCCAGGAAATCGCCGCGATCGACGGCGTCGAACTCGATTCGGAAGTCACTTTC GCCGATCTGACGACCCTCCGCATCGGCGGAAAACCCCGCAGCGCCGTACGTTGCCAGACCACGGAGGCG CTCGTCGTGGCCGACGGCGATCTGGATGTTATTGCCGTCATCATCGAAACCGACGACGTCTCCATCAAC CTCACCGACGGTCTCCTCACCGCCGATGCAGGCGCTGTTTGGGACGATGTTGTCCACCTTTCGGTGGAT GTGGGCGCCTACGGCACGGAAGTTTCCGATGTACTCACCCGCGTCCAGCTTCTCGACCGCACCACCAC CAAGTCTCCTGGGTCGACGCCTCCGAACTCGACCTCTCTTACCGATACTCCAATCTCAAATTCACCAAC CGCGCAGTCGTCTTGGCGATCGAACTCCAGCTCCTCACCGACGGATTGTCCGCGCCGCTACGTTTTGGT GACGCCGTCCTAGAACTCCGCCGCGCCAAAGGCATGGTCGTGGAACACACCGACCACGACACCTGGTCC GCCGGATCCTTCTCACCAACCCAATCGTCGACCCAGCCCTTGCCGACGCAGTCTTTGAAAAAGTCGGC GAACCCACCATGCCCGCTTCCCAGCCGGCGATGGCAAAGAAAACTCTCCGCAGCCTGGCTCATCGAA CGCGCCGGCTTCAAAAAGGGACACCCCGGCGCAGGCGCAAAAGCCTCCCTGAGCACCAAACACACCCTC GCACTCACCAACCGTGGCGACGCCCCGCGCCTCCGACCTCGTCGCATTAGCCAAAGAAATCCGCGACGGA GTCCTCGAAACCTTCGGCGTCACCCTCGTCCCAGAACCCGTCTGGATTGGAATCAGCATCGATGAC

RXS02485 - 3'-Region TGAATTTTCCGACGTCCCTGGCA

RXS02539 - 5'-Region

 ${\tt GGCTGCTAAGCGTGCGAATGTGCGCGTTGTCACAATCGTTGACCAAGTGTCACCTGACGCACAGGTAGTGCTCAGGTGGAGGTGGCCCAAAGGAGACCCA}$

RXS02539 - coding Region

ATGACTGTCTACGCAAATCCAGGAACCGAAGGCTCGATCGTTAACTATGAAAAGCGCTACGAGAACTAC ATTGGTGGCAAGTGGGTTCCACCGGTAGAGGGCCAGTACCTTGAGAACATTTCACCTGTCACTGGTGAA GTTTTCTGTGAGGTCGCACGTGGCACCGCAGCGGACGTGGAGCTTGCACTGGATGCTGCACATGCAGCC GCTGATGCGTGGGGCAAGACTTCTGTCGCTGAACGTGCTCTGATCCTGCACCGCATTGCGGACCGCATG GAAGAGCACCTGGAAGAAATCGCAGTTGCAGAAACCTGGGAGAACGGCAAGGCAGTCCGTGAGACTCTT GCTGCAGATATCCCACTGGCAATCGACCACTTCCGCTACTTTGCTGGCGCGATCCGTGCTCAGGAAGAT CGTTCCTCACAGATCGACCACAACACTGTTGCTTACCACTTCAACGAGCCAATCGGTGTTGTTGGTCAG ATCATTCCTTGGAACTTCCCAATCCTCATGGCTACCTGGAAGCTCGCACCGGCACTTGCTGCAGGTAAC GCGATCGTCATGAAGCCAGCTGAGCAGACCCCAGCATCCATTTTGTATCTGATTAACATCATCGGCGAT CTCATCCCAGAGGGCGTCCTCAACATCGTCAACGGACTCGGCGGTGAAGCAGGCGCTGCACTGTCCGGC TCTAATCGGATTGCCAAGATTGCTTTCACCGGTTCCACCGAGGTCGCCAAGCTGATCAACCGCGCTGCA CTGTCACAGGATGACGCCTTCGCAGAGAAGGCAGTTGAAGGCTTCGCGATGTTCGCCCTCAATCAGGGT GAAGTTTGTACCTGTCCTTCCCGTGCACTTGTTCATGAGTCCATCGCTGATGAATTCCTCGAGCTTGGC GTGAAGCGAGTTCAGAACATCAAGCTGGGTAACCCACTTGATACTGAAACCATGATGGGTGCTCAGGCG TCCCAGGAGCAGATGGACAAGATCTCCTCCTACCTGAAGATCGGCCCAGAAGAAGGCGCTCAAACCCTC ACTGGTGGCAAGGTCAACAGGTTGATGGCATGGAGAACGGTTACTACATTGAGCCAACCGTTTTCCGC GGCACCAACGACATGAGGATCTTCCGCGAGGAAATCTTCGGACCAGTCCTTTCTGTTGCTACCTTCAGC GACTTCGATGAGGCCATCCGTATTGCAAACGACACCAACTACGGCCTCGGCGCTGGTGTCTGGAGCCGT GACCAAAACACCATTTATCGTGCAGGTCGCGCAATCCAGGCTGGTCGAGTTTGGGTCAACCAGTACCAC AACTACCCAGCGCACTCCGCTTTCGGTGGATACAAGGAGTCCGGCATCGGCCGTGAGAACCACCTCATG ATGCTGAACCACTACCAGCAGACCAAGAACCTGTTGGTCTCCTACGATCCAAACCCAACCGGACTGTTC

RXS02539 - 3'-Region TGATCTAAGCGTTAAGTCCTAGA RXS02554 - 5'-Region

GCTTTTGAAGTGTCGCGTGTGCGGACTGAAATAGTTTCCGCTTCAACTTGGTTGCTAAGGATAGGCTCCATAAAAATAACCAAAGGCGGAAAATTTCA

RXS02554 - coding Region

ATGTCACACATTAGCCATCCATTGCCATCCTCGGTGCTGGCCGAGTGGGTTCTTCACTTGCCAGGTCA
GCGGTCGCCGCAGGCTATGAGGTAAAGGTTGCTGGTTCAGGTGCTGTGGACAAAATCGCTCTTACCGCT
GAGATCCTTATGCCCGGCGGGTTCCAAGCACTGCTGACCAGGCTGTAAAGGATGCAGATATTGTGTTC
TTGGCTGTTCCCCTGCATAAATTCCGCAGTGTCAATCCAGCCACTTTAGAGGGCCAAGATCGTTATTGAC
ACGATGAACCACTGGGTTCCGGTCAATGGTGAGTTGGAGGAAATTGATCAGGATCCGCGCAGCACTTCG
GAGATTATTGCGGAGTTTTTCGCGGGATCAACCATGGTGAAGTCTTTTAACCACATTGGTTATCACGAG
ATTGAGCAGGATGCGGGTACCGGGCGTGCGATTGCCTATGCCACGGATGATGTGGATGCAGGTGCCCAG
GTTGCACAGCTAATTAAGAGTTTTTGGGTTTGTTCCTTTAAATATTTGGCGCATTGGAAAACGGCCGTATT
CTGGAACCTGGCCAAGAAGCTTTCGGCGCGCACCTTAATAAAGATTCGCGCCCTAGAACTTGTTAATCAG
CGG

RXS02554 - 3'-Region TAGTACCTCGATCTTCAGCCAAC

RXS02560 - 5'-Region

 ${\tt TTGGGGCAAGCCAGCTAACGCATTTCTTGTGGAAACCGCAGACATTGAGGCCGCCCACGCGGAACTTCTAAGAGCAGTGGAATGAAATAATCCGGTGCTG}\\$

RXS02560 - coding Region

RXS02560 - 3'-Region
TAAAAGCATGATTATGGACGCCT

RXS02578 - 5'-Region

GGCAAAAATGAGGAACAGCACGCCCGCAATAATGAGGACCGTTGCAGATCGCTTCATAAAAAACAGCCCACACCTTTCCGCTAAACTCGCATGTTGAAATA

RXS02578 - coding Region

GTGACGGTCTTGTTGACGATCCCAGTTGCCGCCATCAGCTACACCTTCATCGAAGAGCCCATCAGCGGT GGACCCGGCGCGCATTCAGGCTGGGGGTCGTTAGGATTCACCATTTTTCTGGGGGTAGGTCTGGAAAA

RXS02578 - 3'-Region TGATGAATTGGCACCACGTCAAG

RXS02741 - 5'-Region

 ${\tt ACTGGTCACCTGGTTTGGTCTGCACTCTGACTCCCCTCAAAAGGGCACAATTTGGTCAATTTCCCAACCTTGTCTTTCAGTCATGGTTAGTGTGGGAACC}$

RXS02741 - coding Region

RXS02741 - 3'-Region TAAACACGCATAAAAAGATCCTG

RXS03058 - 5'-Region

ACGAGCTTCCGCTCTGCACAAGCCGCTAGAAGCCCCGCATAGCCCTAATGTAGAGCTCATGCCCATTTGGAATCACAACACCGCATATCGGCCATGGCTG

RXS03058 - coding Region

GTGTCAAAGCTCAAAGGCTCAAGATCGCTTCTCGACGTCGGCTCCGGCGATCACTCCTTCGCCGACCTG
GCCGGCCGCCAGGTCGCCATGTCGATGTCGTGGATCCTCTTATTAATACAACCTTTGAAGAATTCCAG
CCGACCCAAAGCTACGATGCCATCACGTTCATCGCGTCCCTCCATCACATGAACGCGGAAGAAGGACTT
AACAAAGCAGTCCGAATCCTCAATCCTGGCGGCAAGCTCCTCATCGTAGGCCTCGCCAAAAACAAAACC
GCCTCCGACTGGATCATCTCCGGACTACAAGCTTTTCTCTCCCGACCAATCAGCCTCATCAATAGGGAA
CAACAAATCTACCCCTTCCCTACCAAAGAACCCTCAGAGAGTCTCCACGAAATACGACAACTCACCAAG
CAGCTCCTCCCTCACCGCCGTATTCGCCGTGGAATCCACTTCCGATACCTCCTCGAGTGGACAAAGCCT

RXS03058 - 3'-Region TAAACAGCCCTATAAACCAAAAA

RXS03061 - 5'-Region

 $\tt CTGCCACCACTGGTCATTGCAGAGGACACTCTCCGTGATGGTCTTCAGGTGTTAGTCGCAGCCCTAGAGCGCGAAACCGCGCACCAGAAGGTGGGCTAAA$

RXS03061 - coding Region

GTGTCTTTGACCTTCCCAGTAATCAACCCCAGCGATGGCTCCACCATCACCGAGCTAGAAAACCACGAT TCCACCCAGTGGATGTCCGCGCTCTCTGATGCAGTTGCAGCTGGTCCTTCATGGGCTGCGAAAACTCCC CGCGAAAGATCCGTGGTACTCACCGCAATCTTCGAAGCACTGACCGAACGCGCCCAAGAACTTGCAGAG ATCATCCACCTGGAAGCTTGGAAAATCCGATGCAGAAGCTCTTGGTGAAGTCGCTTATGGTGCAGAATAC TTCCGTTGGTTGCGGAAGAAGCAGTGCGCCTGCCCGGCCGCTACGGACAGTCA

RXS03119 - 5'-Region

TGGGAGGTGTCGCACCAAGTACTTTTGCGAAGCGCCATCTGACGGATTTTCAAAAGATGTATATGCTCGGTGCGGAAACCTACGAAAGGATTTTTTACCC

RXS03119 - coding Region

ATGGCTGTATACGAACTCCCAGAACTCGACTACGCATACGACGCTCTCGAGCCACACATCGTCGCTGAA
ATCATGGAGCTTGACCAGTCCAAGGACCACGCAACCTACGTTGCGGGCGCAAATGCAGCACTC

RXS03119 - 3'-Region TAGGCACTAGAGAAGGCACGCGA

RXS03120 - 5'-Region

CTGGGCAGTTCTTGGGTACGACCACATATCCGGTCGCCTGGTTATCGAGCAGCTCACCGACCAGGAGGGCAACATCTCCTTCGACATCACCCCAGTTCTG

RXS03120 - coding Region

RXS03120 - 3'-Region TAAGCATTTTTAGTCCGTGCAAT

RXS03150 - 5'-Region

TTTAACAGAGTGCGTTTCAATGCCTGTAGTGTTCCGGCAATTTTGAATGTCGTTACGGTTACCCAAGGCTGAATTCCTGAGCTCACCTTGTACAAGATCA

RXS03150 - coding Region

RXS03150 - 3'-Region TAATCCAAACTGCACCTATATAT

RXS03218 - 5'-Region

 ${\tt TTGGTACGGGGGTTAACAACCTAGCTTTGTATCTGAAGGCTTCGGAGATTTCCTGTATACATCAACAAT}\\ {\tt TGCCCTTTAACCAGGAGTATTCTTAGCTTCT}$

RXS03218 - coding Region

RXS03218 - 3'-Region TGAGTTCTAGCAAATGGCGGCTTGTTAGTG